

FILE REFERENCE: 97-11C2
CURRENT APPLICATION NUMBER: US/10/716,824
CURRENT FILING DATE: 2003-11-19
PRIOR APPLICATION NUMBER: US/10/082,502
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: 09/318,028
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 09/109,808
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/089,899
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/085,983
PRIOR FILING DATE: 1998-05-19
PRIOR APPLICATION NUMBER: 60/051,704
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 83
TYPE: PRT
ORGANISM: Homo sapiens
US-10-716-824-2

Query Match 100.0%; Score 444; DB 4; Length 83;
Best Local Similarity 100.0%; Pred. No. 1.1e-44;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKGHWLALLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTQMGSPRNP 60
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Db 1 MKGHWLALLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTQMGSPRNP 60
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Qy 61 DGSQSVVEVTVPNNKVAHSGF 83
|||||

Db 61 DGSQSVVEVTVPNNKVAHSGF 83
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RESULT 3
US-10-932-376-2
Sequence 2, Application US/10932376
Publication No. US20050124801A1
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Jelinek, Laura J.
TITLE OF INVENTION: Mammalian Secretory Protein - 9
FILE REFERENCE: 97-11C2
CURRENT APPLICATION NUMBER: US/10/932,376
CURRENT FILING DATE: 2004-09-02
PRIOR APPLICATION NUMBER: US/10/082,502
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: 09/318,028
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 09/109,808
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/089,899
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/085,983
PRIOR FILING DATE: 1998-05-19
PRIOR APPLICATION NUMBER: 60/051,704
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 83
TYPE: PRT
ORGANISM: Homo sapiens
US-10-932-376-2

Query Match 100.0%; Score 444; DB 5; Length 83;
Best Local Similarity 100.0%; Pred. No. 1.1e-44;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKGHWLALLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTQMGSPRNP 60
|||||

Db 1 MKGHWLALLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTQMGSPRNP 60
Qy 61 DGSQSVVEVTVPNNKVAHSGF 83
|||||

Db 61 DGSQSVVEVTVPNNKVAHSGF 83
|||||

RESULT 4

US-09-978-360A-716
Sequence 716, Application US/09978360A
Publication No. US20040110939A1
GENERAL INFORMATION:
APPLICANT: Edwards, Jean-Baptiste Dumas Milne
APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
APPLICANT: Jobert, Severin
APPLICANT: Ciusel, Catherine
TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
FILE REFERENCE: 56.US4.CIP
CURRENT APPLICATION NUMBER: US/09/978,360A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: US 60/066,677
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/069,957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: US 60/074,121
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: US 60/081,563
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: US 60/096,116
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: US 60/099,273
PRIOR FILING DATE: -09-04
PRIOR APPLICATION NUMBER: US 09/191,997
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: US 09/215,435
PRIOR FILING DATE: 1998-12-17
PRIOR APPLICATION NUMBER: PCT/IB98/02122
PRIOR FILING DATE: 1998-12-17
PRIOR APPLICATION NUMBER: US 09/247,155
PRIOR FILING DATE: 1999-02-09
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 810
SOFTWARE: Patent.pm
SEQ ID NO 716
LENGTH: 84
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -20...-1
US-09-978-360A-716

Query Match 100.0%; Score 444; DB 3; Length 84;
Best Local Similarity 100.0%; Pred. No. 1.1e-44;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKGHWLALLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTQMGSPRNP 60
|||||

Db 1 MKGHWLALLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTQMGSPRNP 60
|||||

Qy 61 DGSQSVVEVTVPNNKVAHSGF 83
|||||

Db 61 DGSQSVVEVTVPNNKVAHSGF 83
|||||

RESULT 5

US-10-319-763-204
Sequence 204, Application US/10319763
Publication No. US20030144490A1
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric

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Query Match      100.0%; Score 444; DB 4; Length 84;
Best local Similarity 100.0%; Pred. No, 1.le-44;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MKGNGWLALLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTQMGSFRNP 60
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Db      1  MKGNGWLALLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTQMGSFRNP 60
      |||

Qy      61  DGSQSVVEVTVTVPNNKVAHSGF 83
      |||
Db      61  DGSQSVVEVTVTVPNNKVAHSGF 83
      |||

RESULT 7
US-10-319-763-110
; Sequence 110, Application US/10319763
; Publication No. US20030144490A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: EXTENDED CNAS FOR SECRETED PROTEINS
; FILE REFERENCE: G-031.US04.DIV
; CURRENT APPLICATION NUMBER: US/10/319,763
; PRIORITY FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: 60/066,677
; PRIORITY FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/069,957
; PRIORITY FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/074,121
; PRIORITY FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/081,563
; PRIORITY FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: 60/096,116
; PRIORITY FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/099,273
; PRIORITY FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent.pm
; SEQ ID NO 110
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -20..-1
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 53
; OTHER INFORMATION: Xaa = any one of the twenty amino acids
US-10-319-763-110

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; TYPE: PRNT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -20..-1
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 53
; OTHER INFORMATION: Xaa = any one of the twenty amino acids
US-10-319-763-110

Query Match          92.5%; Score 410.5; DB 4; Length 97;
Best Local Similarity 94.0%; Pred. No. 1.2e-40;
Matches 79; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 MKCGWMLALLGLLGTAWARRSODLHCGACRALVDELEWEIAQVDPKTIQMGSRINP 60
DB 1 MKCGWMLALLGLLGTAWARRSRDLHCGACRALVDELEWEIAQVDPKTIQMGSRINP 60

QY 61 DGSQSVEVTVTYV-PPNKVAHSGF 83
DB 61 DGSQSVEVTVTYXSPKTKVAHSGF 84

RESULT 8
US-09-978-360A-717
; Sequence 717, Application US/09978360A
; Publication No. US20040110939A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste Dumas Milne
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie

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; APPLICANT: Jobert, Severin
; APPLICANT: Clusel, Catherine
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: 56.US4.CIP
; CURRENT APPLICATION NUMBER: US/09/978.360A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: US 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: US 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: US 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 60/099,273
; PRIOR FILING DATE: -09-04
; PRIOR APPLICATION NUMBER: US 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: US 09/215,435
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: PCT/IB98/02122
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: US 09/247,155
; PRIOR FILING DATE: 1999-02-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 810
; SOFTWARE: Patent.pm
; SEQ ID NO 717
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -20...-1
US-09-978-360A-717

Query Match      83.1%; Score 369; DB 3; Length 182;
Best Local Similarity 100.0%; Pred. No. 2.2e-35;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MKGHWLALLGLGTAWARRSODLHCGACRALVDELEWEIAQVDPKTIQMSFRINP 60
Db      1  MKGHWLALLGLGTAWARRSODLHCGACRALVDELEWEIAQVDPKTIQMSFRINP 60

Qy      61  DGSQSVVEV 69
Db      61  DGSQSVVEV 69

RESULT 9
US-10-028-072-174
; Sequence 174, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang

; TITLE OF INVENTION:
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/028,072
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
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; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059836
; PRIOR FILING DATE: 1997-09-24
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062285
; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/063082
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; PRIOR FILING DATE: 1997-10-28
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; PRIOR APPLICATION NUMBER: 60/063733
; PRIOR FILING DATE: 1997-10-29
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; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063738
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063755
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064248
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/064809
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065846
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/066453
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066511
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; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/069212
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069278
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069334
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069694
; PRIOR FILING DATE: 1997-12-16
; PRIOR APPLICATION NUMBER: 60/072320
; PRIOR FILING DATE: 1998-01-23
; PRIOR APPLICATION NUMBER: 60/073612
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: 60/074086
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/074092
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-02-27
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/081203
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081229
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081695
; PRIOR FILING DATE: 1998-04-14
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; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086414
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/086430
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28

; PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088730
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088741
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088810
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 19/98-06-11
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089599
; PRIOR FILING DATE: 1998-06-17
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; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090538
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07

Query Match 83.1%; Score 369; DB 4; Length 182;

Best Local Similarity 100.0%; Pred. No. 2.2e-35;

Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKGHWLALLGALLGTAWARRSODLHCGACRALVDSLEWIEIAQVDPKKTQMGSFRINP 60

Db 1 MKGHWLALLGALLGTAWARRSODLHCGACRALVDSLEWIEIAQVDPKKTQMGSFRINP 60

Qy 61 DGSQSVVEV 69

Db 61 DGSQSVVEV 69

RESULT 10

US-10-140-808-174

; Sequence 174, Application US/10140808

; Publication No. US20030017563A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tamas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3330R1C182

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; CURRENT APPLICATION NUMBER: US/10/140,808
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 174
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-808-174

Query Match      83.1%; Score 369; DB 4; Length 182;
Best Local Similarity 100.0%; Pred. No. 2.2e-35;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKGHWLALLGALLGTAWARRSODLHCGACRALVDELEWIAQVDPKKTQMGSPRNP 60
   |||||||
Db 1 MKGHWLALLGALLGTAWARRSODLHCGACRALVDELEWIAQVDPKKTQMGSPRNP 60
   |||||||

Qy 61 DGSQSVVEV 69
   |||||||
Db 61 DGSQSVVEV 69

RESULT 11
US-10-121-049-174
; Sequence 174, Application US/10121049
; Publication No. US2003002239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C17
; CURRENT APPLICATION NUMBER: US/10/121,049
; CURRENT FILING DATE: 2002-04-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 174
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-121-049-174

Query Match      83.1%; Score 369; DB 4; Length 182;
Best Local Similarity 100.0%; Pred. No. 2.2e-35;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKGHWLALLGALLGTAWARRSODLHCGACRALVDELEWIAQVDPKKTQMGSPRNP 60
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Db 1 MKGHWLALLGALLGTAWARRSODLHCGACRALVDELEWIAQVDPKKTQMGSPRNP 60
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Qy 61 DGSQSVVEV 69
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Db 61 DGSQSVVEV 69

RESULT 12
US-10-123-904-174
; Sequence 174, Application US/10123904
; Publication No. US20030022328A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C54
; CURRENT APPLICATION NUMBER: US/10/123,904
; CURRENT FILING DATE: 2002-04-16
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 174
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-123-904-174

Query Match      83.1%; Score 369; DB 4; Length 182;
Best Local Similarity 100.0%; Pred. No. 2.2e-35;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKGHWLALLGALLGTAWARRSODLHCGACRALVDELEWIAQVDPKKTQMGSPRNP 60
   |||||||
Db 1 MKGHWLALLGALLGTAWARRSODLHCGACRALVDELEWIAQVDPKKTQMGSPRNP 60
   |||||||

Qy 61 DGSQSVVEV 69
   |||||||
Db 61 DGSQSVVEV 69

RESULT 13
US-10-140-470-174
; Sequence 174, Application US/10140470
; Publication No. US20030022331A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C160
; CURRENT APPLICATION NUMBER: US/10/140,470
; CURRENT FILING DATE: 2002-05-06
```

; Prior Application removed - See Palm or File Wrapper

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 174

; LENGTH: 182

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-140-470-174

Query Match 83.1%; Score 369; DB 4; Length 182;

Best Local Similarity 100.0%; Pred. No. 2.2e-35;

Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKGHWLALLGALLGTAWARRSODLHCGACRALVDELEWIAQVDPKKTQMGSRINP 60

Db 1 MKGHWLALLGALLGTAWARRSODLHCGACRALVDELEWIAQVDPKKTQMGSRINP 60

Qy 61 DGSQSVVEV 69

Db 61 DGSQSVVEV 69

RESULT 14

US-10-175-746-174

; Sequence 174, Application US/10175746

; Publication No. US20030027270A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Deanoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P330R1C353

; CURRENT APPLICATION NUMBER: US/10/175,746

; CURRENT FILING DATE: 2002-06-19

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 174

; LENGTH: 182

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-175-746-174

Query Match 83.1%; Score 369; DB 4; Length 182;

Best Local Similarity 100.0%; Pred. No. 2.2e-35;

Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKGHWLALLGALLGTAWARRSODLHCGACRALVDELEWIAQVDPKKTQMGSRINP 60

Db 1 MKGHWLALLGALLGTAWARRSODLHCGACRALVDELEWIAQVDPKKTQMGSRINP 60

Qy 61 DGSQSVVEV 69

Db 61 DGSQSVVEV 69

RESULT 15

US-10-176-918-174

; Sequence 174, Application US/10176918

; Publication No. US20030027275A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Deanoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P330R1C382

; CURRENT APPLICATION NUMBER: US/10/176,918

; CURRENT FILING DATE: 2002-06-20

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 174

; LENGTH: 182

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-176-918-174

Query Match 83.1%; Score 369; DB 4; Length 182;

Best Local Similarity 100.0%; Pred. No. 2.2e-35;

Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKGHWLALLGALLGTAWARRSODLHCGACRALVDELEWIAQVDPKKTQMGSRINP 60

Db 1 MKGHWLALLGALLGTAWARRSODLHCGACRALVDELEWIAQVDPKKTQMGSRINP 60

Qy 61 DGSQSVVEV 69

Db 61 DGSQSVVEV 69

Qy 61 DGSQSVVEV 69

Db 61 DGSQSVVEV 69

Search completed: May 8, 2006, 21:12:01

Job time : 170 secs

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 8, 2006, 20:49:24 ; Search time 186 Seconds
(without alignments)
196.067 Million cell updates/sec

Title: US-10-716-824-2
Perfect score: 444
Sequence: 1 MKGHWLALLGALLGTAWA.....QSVVEVTVTVPKVAHSGF 83

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	444	100.0	83	3 AAY15130	Aay15130 Human Zsi
2	444	100.0	84	2 AAW88469	Aaw88469 Human sec
3	444	100.0	84	2 AAY36199	Aay36199 Human sec
4	444	100.0	84	6 ADA57311	Ada57311 Human sec
5	444	100.0	84	7 ADC74386	Adc74386 Human sec
6	444	100.0	84	7 ADD38010	Add38010 Human sec
7	444	100.0	84	7 ADJ46051	Adj46051 Novel hum
8	444	100.0	84	8 ADP19460	Adp19460 Human sec
9	444	100.0	85	2 AAY30716	Aay30716 Amino aci
10	410.5	92.5	97	2 AAY36152	Aay36152 Human sec
11	410.5	92.5	97	7 ADJ45957	Adj45957 Novel hum
12	369	83.1	168	8 ADP29267	Adp29267 Human sec
13	369	83.1	182	2 AAW88474	Aaw88474 Human sec
14	369	83.1	182	2 AAY36200	Aay36200 Human sec
15	369	83.1	182	3 AAY15135	Aay15135 Human Zsi
16	369	83.1	182	3 AAY52391	Aay52391 Human tra
17	369	83.1	182	4 AAU12258	Aau12258 Human PRO
18	369	83.1	182	5 AAU97063	Aau97063 Transmemb
19	369	83.1	182	5 ABB09717	Abb09717 Amino aci
20	369	83.1	182	6 ABO17702	Abo17702 Novel hum
21	369	83.1	182	6 ADA56723	Ada56723 Human sec
22	369	83.1	182	6 ABU80956	Abu80956 Human PRO
23	369	83.1	182	6 ABU66656	Abu66656 Human PRO
24	369	83.1	182	6 ABU59737	Abu59737 Novel sec

ALIGNMENTS

RESULT 1
AAY15130
ID AAY15130 standard; protein; 83 AA.
XX
AC AAY15130;
XX
DT 07-FEB-2000 (first entry)
XX
DE Human Zsig9 secretory protein partial sequence.
XX
KW Secretory protein-9; Human Zsig9; chromosome 12q15 region; tumour;
KW overexpression; antagonist; antibody; antisense nucleotide; detection;
KW treatment; receptor; radio-label; fusion; polypeptide toxin; technique;
KW down-regulation; probe; diagnostic; therapeutic; cancer; brain; liver;
KW stomach; lymphoma.
XX
OS Homo sapiens.
XX
Key Location/Qualifiers
FH Peptide 1..20
FT /label= Signal_sequencá
FT Protein 21..83
FT /label= Mature_Zsig9_secretory_protein
FT /note= "The sequence according to the specification has
84 amino acids, but only 83 amino acids are shown in the
sequence listing"
WO9960405-A1.
25-NOV-1999.
19-MAY-1999; 99WO-US011107.
19-MAY-1998; 98US-00081183.
(ZYMO) ZYMOGENETICS INC.
Moore EE, Taft DW;
WPI; 2000-039447/03.
N-PSDE; AAZ08284.
Detecting tumors using antibodies, antagonists and antisense nucleotides
to secretory protein-9 (Zsig9).
Claim 1; Page 30; 45pp; English.
XX

25 369 83.1 182 6 ABO24927 Human sec
26 369 83.1 182 6 ABU66932 Human sec
27 369 83.1 182 6 ADA45693 Novel hum
28 369 83.1 182 6 ADA76124 Human PRO
29 369 83.1 182 6 ADA18774 Human PRO
30 369 83.1 182 6 ADA61397 Homo sapi
31 369 83.1 182 6 ADB19182 Novel hum
32 369 83.1 182 6 ADB27723 Human PRO
33 369 83.1 182 6 ADA86202 Novel hum
34 369 83.1 182 6 ADB15766 Human PRO
35 369 83.1 182 6 ADA47552 Human PRO
36 369 83.1 182 6 ADA67347 Human PRO
37 369 83.1 182 6 ADB30354 Human PRO
38 369 83.1 182 6 ADA85650 Novel hum
39 369 83.1 182 6 ADA96862 Human PRO
40 369 83.1 182 6 ADA79166 Human PRO
41 369 83.1 182 6 ADA87305 Novel hum
42 369 83.1 182 6 ADB16507 Human PRO
43 369 83.1 182 6 ADA91599 Novel hum
44 369 83.1 182 6 ADB14662 Human PRO
45 369 83.1 182 6 ADB18623 Novel hum

CC The present protein sequence is the secretory protein-9, Zsig9. This
 CC sequence is mapped to the human chromosome 12q15 region. It is
 CC overexpressed in tumours. Antagonists, antibodies and antisense
 CC nucleotides to Zsig9 are useful for detecting and treating tumours. The
 CC antagonist may be an antibody or receptor to Zsig9 and it may be radio-
 CC labelled or fused to a polypeptide toxin. It can be used for down-
 CC regulating the overexpression of Zsig9. The gene sequence can be used as
 CC nucleic acid probes to detect RNA encoding Zsig9. The Zsig9 sequence
 CC facilitates improved diagnostic and therapeutic techniques for detecting
 CC and treating cancers, especially of the brain, liver, stomach, lymphoma
 CC etc., at an early stage
 CC
 SQ Sequence 83 AA;
 Query Match 100.0%; Score 444; DB 3; Length 83;
 Best Local Similarity 100.0%; Pred. No. 4.3e-47;
 Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKGNGWLALLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTIQMSFRINP 60
 DB 1 MKGNGWLALLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTIQMSFRINP 60
 QY 61 DGSQSVVEVTVPNNKVAHSGF 83
 DB 61 DGSQSVVEVTVPNNKVAHSGF 83
 RESULT 2
 AAW88469
 ID AAW88469 standard; protein; 84 AA.
 XX
 AC AAW88469;
 DT 10-MAY-1999 (first entry)
 XX
 DE Human secretory peptide-9 (Zsig9).
 XX
 KW Secretory peptide-9; Zsig9; human; tumour marker; cancer; therapy;
 KW diagnosis; growth enhancer.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FH Peptide 1..20
 FT /note= "signal peptide"
 FT Protein 21..84
 FT /note= "mature protein"
 FT Disulfide-bond 28..31
 XX
 PN WO9901554-A1,
 XX
 PD 14-JAN-1999.
 XX
 PF 02-JUL-1998; 98WO-US013859.
 XX
 PR 03-JUL-1997; 97US-0051704P.
 PR 03-JUL-1997; 97US-0088088.
 PR 19-MAY-1998; 98US-00081338.
 PR 19-MAY-1998; 98US-0085983P.
 PR 17-JUN-1998; 98US-00099005.
 PR 17-JUN-1998; 98US-0089899P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Sheppard PO, Jelinek LJ, Jaspers SR, Whitmore TE;
 DR N-PSDB; AAX06968.
 DR WPI; 1999-106055/09.
 XX
 XX New mammalian secretory peptide-9 (Zsig9) - used as a growth enhancer for
 PT placenta, liver and heart, and as an indicator of cancer.
 XX
 PS Claim 8; Page 67; 85pp; English.

XX This is the amino acid sequence of novel human secretory peptide-9, or
 CC Zsig9, a polypeptide that is overexpressed in a number of human tumours
 CC including brain, liver, lung, oesophageal, stomach, colon, rectal,
 CC thyroid and lymphoma tumors. Thus, Zsig can be used as an indicator for
 CC cancer. Zsig9 cDNA (see AAX06968) was discovered in a placenta clone from
 CC a full-term pregnancy cDNA library. The invention provides Zsig9
 CC polypeptides (see AAW88469-77) including mature polypeptides, other
 CC processed forms, variants and mouse orthologues, and polynucleotides (see
 CC AAX06968-70) encoding them. Antibodies raised against Zsig9 can be used
 CC as diagnostic agents to determine the presence of Zsig9, and thus the
 CC presence of cancer. They can also be labelled with radioisotopes or fused
 CC with toxins and used to treat tumours which overexpress Zsig9. Antisense
 CC nucleotides derived from Zsig9 cDNA can also be used to inhibit the
 CC growth of tumour cells. Zsig9 proteins can be used to enhance the growth
 CC or development of the placenta, heart or liver
 XX
 SQ Sequence 84 AA;
 Query Match 100.0%; Score 444; DB 2; Length 84;
 Best Local Similarity 100.0%; Pred. No. 4.4e-47;
 Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKGNGWLALLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTIQMSFRINP 60
 DB 1 MKGNGWLALLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTIQMSFRINP 60
 QY 61 DGSQSVVEVTVPNNKVAHSGF 83
 DB 61 DGSQSVVEVTVPNNKVAHSGF 83
 RESULT 3
 AAY36199
 ID AAY36199 standard; protein; 84 AA.
 XX
 AC AAY36199;
 DT 23-SEP-1999 (first entry)
 XX
 DE Human secreted protein #71.
 XX
 KW Secreted protein; human; cytostatic; thrombotic; osteopathic; forensic;
 KW diagnostic; gene therapy; chromosome mapping; secretion vector.
 XX
 OS Homo sapiens.
 XX
 PN WO9925825-A2.
 XX
 PD 27-MAY-1999.
 XX
 PF 13-NOV-1998; 98WO-IB001862.
 XX
 PR 13-NOV-1997; 97US-0066677P.
 PR 17-DEC-1997; 97US-0069957P.
 PR 09-FEB-1998; 98US-0074121P.
 PR 13-APR-1998; 98US-0081563P.
 PR 10-AUG-1998; 98US-00961116P.
 PR 04-SEP-1998; 98US-0099273P.
 XX
 PA (GEST) GENSET.
 XX
 PI Bougueleret L, Duclert A, Dumas Milne Edwards J;
 DR WPI; 1999-347472/29.
 DR N-PSDB; AAX97883.
 XX
 XX Extended cDNAs encoding secreted proteins.
 PS Claim 7; Page 298-299; 307pp; English.
 XX
 XX AAY36129-Y36222 represent novel human secreted proteins encoded by the
 CC extended cDNA sequences represented in AAX97813-X97906. The proteins of

CC the invention have cytostatic, thrombotic and osteopathic activity. The
 CC extended cDNAs can be used to express secreted proteins or parts of them
 CC or to obtain antibodies capable of binding to the secreted proteins. They
 CC may also be used in diagnostic, forensic, gene therapy and chromosome
 CC mapping procedures. Uses also include design of expression vectors and
 CC secretion vectors

XX Sequence 84 AA;

Query Match 100.0%; Score 444; DB 2; Length 84;
 Best Local Similarity 100.0%; Pred. No. 4.4e-47;
 Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKGHWLALLGALLGTAWARRSODLHCGACRALVDELEWIAQVDPKKTQMGSRINP 60

Db 1 MKGHWLALLGALLGTAWARRSODLHCGACRALVDELEWIAQVDPKKTQMGSRINP 60

Qy 61 DGSQSVVEVTVPNKAHSGF 83

Db 61 DGSQSVVEVTVPNKAHSGF 83

RESULT 4

ID ADA57311 standard; protein; 84 AA.

XX ADA57311;

XX 20-NOV-2003 (first entry)

XX Human secreted protein #5.

XX immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;
 KW cystostatic; cerebroprotective; neuroprotective; nontropic;
 KW cardiovascular; antiarteriosclerotic; gene therapy;

KW human secreted protein; immune disorder; inflammation;

KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;

KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;

KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;

KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;

KW triple helix formation; antisense gene therapy; forensic biology.

XX Homo sapiens.

XX WO2002102994-A2.

XX 27-DEC-2002.

XX 19-MAR-2002; 2002WO-US008278.

XX 21-MAR-2001; 2001US-0277340P.

XX 19-JUL-2001; 2001US-0306171P.

XX 13-NOV-2001; 2001US-0331287P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM;

XX WPI; 2003-167512/16.

XX N-FSDB; ADA56415.

XX New human secreted polypeptides and polynucleotides, useful for
 PT diagnosing, treating or preventing e.g. immune disorders, inflammatory
 PT conditions, respiratory disorders, cancers, CNS disorders, or
 PT neurodegenerative disorders.

XX Claim 13; SEQ ID NO 1501; 1754pp; English.

XX The invention relates to 592 new human secreted polypeptides useful for
 CC diagnosing, treating or preventing e.g. immune disorders, inflammatory
 CC conditions, respiratory disorders, cancers, CNS disorders, or
 CC neurodegenerative disorders, or polypeptides comprising an amino acid
 CC sequence at least 95% identical to the new sequences. The polypeptides,

CC antibodies or antibody fragments that bind to the polypeptides, nucleic
 CC acids encoding the polypeptides, agonists or antagonists that binds to
 CC the polypeptide, are useful in preparing diagnostic or pharmaceutical
 CC compositions for diagnosing, treating or preventing an e.g. immune
 CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,
 CC nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
 CC allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
 CC (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative
 CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and
 CC polynucleotides are useful for chromosome identification, chromosome
 CC mapping, for controlling gene expression through triple helix formation
 CC or antisense DNA or RNA, in gene therapy, for identifying individuals
 CC from minute biological samples, in forensic biology, and as hybridization
 CC probes. The polypeptides are useful for as molecular weight markers on
 CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
 CC gels, to raise antibodies, for testing biological activities, and for
 CC treating or preventing neural disorders, immune system disorders,
 CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
 CC renal, proliferative and/or cancerous diseases. This sequence corresponds
 CC to one of the polypeptide of the invention. Note: The sequence data for
 CC this patent did form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 84 AA;

Query Match 100.0%; Score 444; DB 6; Length 84;

Best Local Similarity 100.0%; Pred. No. 4.4e-47;

Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKGHWLALLGALLGTAWARRSODLHCGACRALVDELEWIAQVDPKKTQMGSRINP 60

Db 1 MKGHWLALLGALLGTAWARRSODLHCGACRALVDELEWIAQVDPKKTQMGSRINP 60

Qy 61 DGSQSVVEVTVPNKAHSGF 83

Db 61 DGSQSVVEVTVPNKAHSGF 83

RESULT 5

ID ADC74386

AD ADC74386 standard; protein; 84 AA.

XX AC ADC74386;

XX 01-JAN-2004 (first entry)

XX Human secreted protein - SEQ ID 1019.

XX antianaemic; antirheumatic; antiarthritic; antiinflammatory; antithyroid;
 KW antidiabetic; immunosuppressive; dermatological; nephrotropic;
 KW antiparkinsonian; neuroprotective; nontropic; antibacterial; virucide;
 KW fungicide; antiparasitic; antiarteriosclerotic; vulnerary; cytostatic;
 KW haemopoietic; haematologic; anaemia; autoimmune disorder;
 KW rheumatoid arthritis; inflammation; Grave's disease; diabetes;
 KW systemic lupus erythematosus; glomerulonephritis; neurodegenerative;
 KW Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis;
 KW cancer; bacterial; viral; fungal; parasitic infection; gene therapy;
 KW human.

XX Homo sapiens.

XX WO2003038063-A2.

XX 08-MAY-2003.

XX 19-MAR-2002; 2002WO-US008277.

XX 21-MAR-2001; 2001US-0277340P.

XX 19-JUL-2001; 2001US-0306171P.

XX 13-NOV-2001; 2001US-0331287P.

PA (HUMA-) HUMAN GENOME SCI INC.
 PI Rosen CA, Ruben SM;
 XX WPI; 2003-430516/40.
 XX DR N-PSDB; ADC73771.
 XX PT New human secreted polypeptide for diagnosing, preventing or treating
 XX PT hematopoietic or hematologic disorders (e.g. anemia), autoimmune
 XX PT disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer or
 XX PT atherosclerosis).
 XX PS Claim 16; SEQ ID NO 1019; 2272pp; English.
 XX CC The invention relates to a novel human secreted polypeptide comprising a
 CC defined sequence given in the specification. The polypeptide, nucleic
 CC acid molecule, antibody, agonist or antagonist of the invention may be
 CC useful for preparing a composition for diagnosing or treating a
 CC haematopoietic or haematologic disorder such as anaemia, autoimmune
 CC disorders such as rheumatoid arthritis, inflammation, Grave's disease,
 CC diabetes, systemic lupus erythematosus or glomerulonephritis,
 CC neurodegenerative disorders including Parkinson's disease and Alzheimer's
 CC disease, wounds and hyperproliferative disorders including
 CC atherosclerosis or cancer, as well as bacterial, viral, fungal or
 CC parasitic infections. The polypeptide may also be used during gene
 CC therapy procedures and for identifying a binding partner by contacting
 CC the polypeptide with a binding partner and determining whether the
 CC binding partner increases or decreases the activity of the polypeptide.
 CC The current sequence is that of the human secreted protein of the
 CC invention.
 XX CC
 XX SQ Sequence 84 AA;
 Query Match 100.0%; Score 444; DB 7; Length 84;
 Best Local Similarity 100.0%; Pred. No. 4.4e-47;
 Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKGHWLALLGALLGTAWARRSQDLHCGACRALVDELEWIEIAQVDPKKTQMGSFRINP 60
 DB 1 MKGHWLALLGALLGTAWARRSQDLHCGACRALVDELEWIEIAQVDPKKTQMGSFRINP 60
 QY 61 DGSQSVVEVTVPNKNVAHSGF 83
 DB 61 DGSQSVVEVTVPNKNVAHSGF 83
 RESULT 6
 ID ADD38010 standard; protein; 84 AA.
 XX AC ADD38010;
 XX DT 15-JAN-2004 (first entry)
 XX DE Human secreted protein #193.
 XX KW human secreted protein; Antiallergic; Antiinflammatory; Antibacterial;
 KW Anti-HIV; Cytostatic; Immunosuppressive; Hemostatic.
 XX OS Homo sapiens;
 XX PN WO200290526-A2.
 XX FD 14-NOV-2002.
 XX PF 19-MAR-2002; 2002WO-US008279.
 XX PR 21-MAR-2001; 2001US-0277340P.
 PR 19-JUL-2001; 2001US-0306171P.
 PR 13-NOV-2001; 2001US-0331287P.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX XX

PI Rosen CA, Ruben SM;
 XX WPI; 2003-140218/13.
 XX PT New human secreted proteins and nucleic acid molecules, useful for
 XX PT preparing a diagnostic or pharmaceutical composition for diagnosing or
 XX PT treating allergic or asthmatic disorders, or related immediate
 XX PT hypersensitivity disorders.
 XX PS Claim 1; SEQ ID NO 492; 1323pp; English.
 XX CC The present invention relates to an isolated polypeptide or human
 CC secreted protein. The polypeptides, nucleic acid molecules, antibodies or
 CC their fragments, and agonists or antagonists that bind are useful for
 CC preparing a diagnostic or pharmaceutical composition for diagnosing or
 CC treating allergic or asthmatic disorders. The polypeptide is also useful
 CC for identifying a binding partner by contacting the polypeptide with a
 CC binding partner, and determining whether the binding partner increases or
 CC decreases the activity of the polypeptide. The polypeptides and nucleic
 CC acid molecules are also useful for detecting, preventing, diagnosing,
 CC prognosticating, treating or ameliorating inflammatory disorders
 CC neoplastic diseases, wound healing and disorders of epithelial cell
 CC proliferation, immune disorders, cardiovascular disorders, blood-related
 CC disorders, infectious diseases, endocrine disorders, or gastrointestinal
 CC disorders. The nucleic acids are also useful for chromosome
 CC identification, radiation hybrid mapping or long-range restriction
 CC mapping, as molecular weight markers or as hybridization or diagnostic
 CC probes. The polypeptides and antibodies are useful for providing
 CC immunological probes for differential identification of the tissues
 CC immunohistochemistry assays. The present sequence represents a human
 CC secreted protein.
 XX CC
 XX SQ Sequence 84 AA;
 Query Match 100.0%; Score 444; DB 7; Length 84;
 Best Local Similarity 100.0%; Pred. No. 4.4e-47;
 Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKGHWLALLGALLGTAWARRSQDLHCGACRALVDELEWIEIAQVDPKKTQMGSFRINP 60
 DB 1 MKGHWLALLGALLGTAWARRSQDLHCGACRALVDELEWIEIAQVDPKKTQMGSFRINP 60
 QY 61 DGSQSVVEVTVPNKNVAHSGF 83
 DB 61 DGSQSVVEVTVPNKNVAHSGF 83
 RESULT 7
 ID ADJ46051 standard; protein; 84 AA.
 XX AC ADJ46051;
 XX DT 06-MAY-2004 (first entry)
 XX DE Novel human secreted protein-related protein sequence SeqID204.
 XX KW secreted protein; upstream regulator; gene therapy; protein purification;
 KW protein synthesis; chromosomal mapping; individual identification;
 KW forensic; hereditary disease; drug reaction; immunoassay;
 KW epitope mapping; vaccine; immune system regulation;
 KW haematopoietic system; tissue growth; reproductive hormone;
 KW cell migration; blood clotting; receptor/ligand interaction;
 KW adhesion molecule; assisted drug delivery;
 KW human glial maturation factor gamma-2; neurite outgrowth;
 KW neurite resprouting; human.
 XX OS Homo sapiens.
 XX PN US2003144490-A1.
 XX FD 31-JUL-2003.
 XX XX

PF 10-DEC-2002; 2002US-00319763.
XX
PR 13-NOV-1997; 97US-0066677P.
PR 17-DEC-1997; 97US-0069957P.
PR 09-FEB-1998; 98US-0074121P.
PR 13-APR-1998; 98US-0081563P.
PR 10-AUG-1998; 98US-0096118P.
PR 04-SEP-1998; 98US-0099273P.
PR 13-NOV-1998; 98US-00191997.
PR 15-SEP-2000; 2000US-00663600.
XX
PA (EDWA/) EDWARDS J D M.
PA (DUCL/) DUCLERT A.
PA (BOUG/) BOUGUELERET L.
XX
PI Edwards JDM, Duclert A, Bougueleret L;
XX
XX WPI; 2003-851788/79.
XX N-PSDB; ADJ46004.
XX
PT New nucleic acid encoding secreted human polypeptides, useful e.g. in
PT gene therapy or diagnosis, also encoded proteins, potential therapeutic
PT agents.
XX
XX Claim 11; SEQ ID NO 204; 269pp; English.
XX
XX This invention relates to novel purified isolated polynucleotides which
XX comprise a sequence that encodes at least 10 amino acids (aa) from any of
XX 48 secreted polypeptide sequences, given in the specification, or
XX fragments of polypeptides encoded by human cDNA contained in the
XX corresponding deposited clone. The DNA sequences of the invention encode
XX secreted proteins (or their fragments) and can be used to
XX identify/isolate upstream regulators, potentially useful in gene therapy
XX or protein purification, by controlling protein synthesis, as probes for
XX chromosomal mapping, identification of individuals, and for diagnosis or
XX forensics, for example identifying genes associated with hereditary
XX diseases or drug reactions, for recombinant expression of the encoded
XX proteins or, where the DNA sequence encodes a signal peptide, for
XX directing secretion of heterologous polypeptides. Polypeptides encoded by
XX the DNA sequences of the invention can be used to raise antibodies,
XX useful for detecting the polypeptide, as (ant)agonists, or for preparing
XX anti-idiotypic antibodies, as tags in for example immunoassays, epitope
XX mapping or vaccines, also as molecular weight markers, to screen for
XX agents with biological activity and as therapeutic agents with,
XX potentially, a very wide range of activities, for example regenerative
XX the immune or haematopoietic systems, tissue growth, reproductive
XX hormones, cell migration, blood clotting or receptor/ligand interaction,
XX also as adhesion molecules for assisted drug delivery. A typical isolated
XX sequence is human glial maturation factor gamma-2, which stimulates
XX neurite outgrowth and resprouting. The present sequence is that of a
XX human secreted protein of the invention.
XX
SQ Sequence 84 AA;
Query Match 100.0%; Score 444; DB 7; Length 84;
Best Local Similarity 100.0%; Pred. No. 4.4e-47;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKGKWLALLIGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTQMGSFRINP 60
Db 1 MKGKWLALLIGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTQMGSFRINP 60
Qy 61 DGSQSVVEVTVPNKNVAHSGF 83
Db 61 DGSQSVVEVTVPNKNVAHSGF 83
RESULT 8
ADP19460
ID ADP19460 standard; protein; 84 AA.
XX
AC ADP19460;
XX

DT 26-AUG-2004 (first entry)
XX
DE Human secreted polypeptide #311.
XX
KW Human; secreted protein; genetic disease.
XX
OS Homo sapiens.
XX
PN US2004110939-A1.
XX
PD 10-JUN-2004.
XX
PF 15-OCT-2001; 2001US-00978360.
XX
PR 17-DEC-1998; 98WO-IB002122.
PR 09-FEB-1999; 99WO-IB000282.
PR 21-JUN-2000; 2000WO-IB000951.
PR 15-SEP-2000; 2000US-00663600.
XX
PA (GEST) GENSET SA.
XX
PI Dumas Milne Edwards J, Bougueleret L, Jobert S, Clusel C;
PI Duclert A;
XX
DR WPI; 2004-440404/41.
DR N-PSDB; ADP19055.
XX
XX New isolated polynucleotide encoding secreted polypeptide, useful for
XX gene therapy, or in diagnostic procedures to identify individuals having
XX genetic diseases resulting from abnormal expression of the genes.
XX
PS Claim 2; SEQ ID NO 716; 113pp; English.
XX
XX The invention relates to human cDNA sequences that encode human secreted
XX proteins. The invention also relates to an antibody that specifically
XX binds to a polypeptide of the invention and a method of binding the
XX polypeptide to an antibody. The polynucleotides are useful for expressing
XX the entire secreted proteins which they encode and for distinguishing
XX human tissues and cells from non-human tissues and cells, and for
XX distinguishing between human tissues and cells that do or do not express
XX the polynucleotides comprising the cDNAs. The polynucleotides and
XX polypeptides are useful in forensic procedures or diagnostic procedures
XX to identify individuals with genetic diseases resulting from abnormal
XX expression of the genes corresponding to the cDNAs. The sequences are
XX also useful in gene therapy to control or treat genetic diseases. This
XX sequence represents a human secreted polypeptide of the invention. Note:
XX The sequence data for this patent did not form part of the printed
XX specification but was obtained in electronic format from USPTO at
XX seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 84 AA;
Query Match 100.0%; Score 444; DB 8; Length 84;
Best Local Similarity 100.0%; Pred. No. 4.4e-47;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKGKWLALLIGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTQMGSFRINP 60
Db 1 MKGKWLALLIGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTQMGSFRINP 60
Qy 61 DGSQSVVEVTVPNKNVAHSGF 83
Db 61 DGSQSVVEVTVPNKNVAHSGF 83
RESULT 9
AAY30716
ID AAY30716 standard; protein; 85 AA.
XX
AC AAY30716;
XX
XX 18-NOV-1999 (first entry)
XX

XX DT 23-SEP-1999 (first entry)
 XX DE Human secreted protein #72.
 XX KW Secreted protein; human; cytostatic; thrombotic; osteopathic; forensic;
 XX KW diagnostic; gene therapy; chromosome mapping; secretion vector.
 XX OS Homo sapiens.
 XX PN W09925825-A2.
 XX PD 27-MAY-1999.
 XX PF 13-NOV-1998; 98W0-IB001862.
 XX PR 13-NOV-1997; 97US-0066677P.
 XX PR 17-DEC-1997; 97US-0069957P.
 XX PR 09-FEB-1998; 98US-0074121P.
 XX PR 13-APR-1998; 98US-0081563P.
 XX PR 10-AUG-1998; 98US-0096116P.
 XX PR 04-SEP-1998; 98US-0099273P.
 XX PA (GEST) GENSET.
 XX PI Bougueleret L, Duciart A, Dumas Milne Edwards J;
 XX DR WPI; 1999-347472/29.
 XX DR N-PSDB; AAX97884.
 XX PT Extended cDNAs encoding secreted proteins.
 XX PS Claim 7; Page 299; 307pp; English.
 XX CC AAY36129-V36222 represents novel human secreted proteins encoded by the
 CC the invention have cytostatic, thrombotic and osteopathic activity. The
 CC extended cDNAs can be used to express secreted proteins or parts of them
 CC or to obtain antibodies capable of binding to the secreted proteins. They
 CC may also be used in diagnostic, forensic, gene therapy and chromosome
 CC mapping procedures. Uses also include design of expression vectors and
 CC secretion vectors
 XX SQ Sequence 182 AA;
 Query Match 83.1%; Score 369; DB 2; Length 182;
 Best Local Similarity 100.0%; Pred. No. 2.5e-37;
 Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MKGHWLALLGALLGTAWARRSQDLHCGACRALVDELEWIEIAQVDPKTTIQMGSRINP 60
 Db 1 MKGHWLALLGALLGTAWARRSQDLHCGACRALVDELEWIEIAQVDPKTTIQMGSRINP 60
 Qy 61 DGSQSVVEV 69
 Db 61 DGSQSVVEV 69
 RESULT 15
 AAY15135
 ID AAY15135 standard; protein; 182 AA.
 XX AC AAY15135;
 XX DT 07-FEB-2000 (first entry)
 XX DE Human Zsig9 secretory protein variant-4.
 XX KW Secretory protein-9; Human Zsig9; chromosome 12q15 region; variant;
 KW overexpression; antagonist; antibody; antisense nucleotide; tumour;
 KW treatment; receptor; radio-label; fusion; polypeptide toxin; technique;
 KW down-regulation; probe; diagnostic; therapeutic; cancer; liver;
 KW detection; stomach; lymphoma; alternative splicing; allelic variation;

KW silent mutation.
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Peptide 1..20
 FT Protein /label= Signal_sequence
 FT /label= Mature Zsig9 protein variant-4
 FT /note= "Overexpressed in tumours"
 XX PN W09960405-A1.
 XX PD 25-NOV-1999.
 XX PF 19-MAY-1999; 99W0-US011107.
 XX PR 19-MAY-1998; 98US-00081183.
 XX PA (ZYMO) ZYMOGENETICS INC.
 XX PI Moore EE, Taft DW;
 XX DR WPI; 2000-039447/03.
 XX DR N-PSDB; AAZ08293.
 XX PT Detecting tumors using antibodies, antagonists and antisense nucleotides
 XX PT to secretory protein-9 (Zsig9).
 XX PS Disclosure; Page 35; 45pp; English.
 XX CC The present sequence is a variant of the secretory protein-9, Zsig9 that
 CC arises due to alternative splicing, allelic variation or silent mutations
 CC that result in amino acid changes. This sequence is mapped to the human
 CC chromosome 12q15 region. It is overexpressed in tumours. Antagonists,
 CC antibodies and antisense nucleotides to Zsig9 are useful for detecting
 CC and treating tumours. The antagonist may be an antibody or receptor to
 CC Zsig9 and it may be radio-labelled or fused to a polypeptide toxin. It
 CC can be used for down regulating the overexpression of Zsig9. The gene
 CC sequence can be used as nucleic acid probes to detect RNA encoding Zsig9.
 CC The Zsig9 sequence facilitates improved diagnostic and therapeutic
 CC techniques for detecting and treating cancers, especially of the brain,
 CC liver, stomach, lymphoma etc., at an early stage
 XX SQ Sequence 182 AA;
 Query Match 83.1%; Score 369; DB 3; Length 182;
 Best Local Similarity 100.0%; Pred. No. 2.5e-37;
 Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MKGHWLALLGALLGTAWARRSQDLHCGACRALVDELEWIEIAQVDPKTTIQMGSRINP 60
 Db 1 MKGHWLALLGALLGTAWARRSQDLHCGACRALVDELEWIEIAQVDPKTTIQMGSRINP 60
 Qy 61 DGSQSVVEV 69
 Db 61 DGSQSVVEV 69
 Search completed: May 8, 2006, 20:52:57
 Job time : 189 secs

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OM protein - protein search, using sw model

Run on: May 8, 2006, 20:49:59 ; Search time 227 Seconds
(without alignments)
257.968 Million cell updates/sec

Title: US-10-716-824-2

Perfect score: 444

Sequence: 1 MKGKGWLLALLGALLGTAWA.....QSVVEVTVTVPNNKVAHSGF 83

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	369	83.1	182	1	MSAP HUMAN
2	361	81.3	182	1	MSAP MOUSE
3	253	57.0	184	2	Q6GPD6 XENLA
4	253	57.0	184	2	Q4KLC8 XENLA
5	215.5	48.5	184	2	Q4SS46 TETNG
6	161.5	36.4	181	2	Q5M7P4 XENLA
7	125.5	28.3	192	2	Q5L1S6 CAEBR
8	123	27.7	193	2	Q5V5P4 DROME
9	96	21.6	189	2	Q3V5P4 DROME
10	87	19.6	187	2	Q7PPM0 ANOGA
11	75.5	17.0	146	2	Q8XVW7 RALSO
12	75.5	17.0	327	2	Q67K51 SYMTH
13	74	16.7	299	2	Q94RE3 LITFO
14	72.5	16.3	377	1	PGES2 HUMAN
15	71.5	16.1	238	2	Q7Q4F3 ANOGA
16	71.5	16.1	335	2	Q9SM22 VANPL
17	70.5	15.9	375	2	Q7TXS8 MYCBO
18	70.5	15.9	375	2	P16333 MYCBO
19	70.5	15.9	384	1	PGES2 MOUSE
20	70.5	15.9	595	2	Q5EK30 VIBCH
21	70.5	15.9	731	2	Q7UQK4 RHOBH
22	70	15.8	353	2	Q7QTC5 GIALA
23	70	15.8	1871	2	Q8M7P9 GIALA
24	69.5	15.7	168	2	Q6T512 TABSO
25	69.5	15.7	566	2	Q926R8 LISIN
26	69	15.5	181	2	Q91148 PSEAE
27	69	15.5	291	2	Q5KZL8 GEOKA
28	69	15.5	593	2	Q9FJ00 ARATH
29	68.5	15.4	152	2	Q9W4C2 DROME
30	68	15.3	150	2	Q7U2B4 RHOBH
31	68	15.3	162	2	Q9KM23 VIBCH

32	68	15.3	311	2	Q9G3Z6 LITFO	Q9G3Z6 lithobius f
33	68	15.3	789	2	Q5F3L1 CHICK	Q5F3L1 gallus gall
34	68	15.3	821	2	Q4RTV2 TETNG	Q4RTV2 tetraodon n
35	67.5	15.2	236	2	Q5QY25 IDILO	Q5QY25 idiomarina
36	67.5	15.2	337	2	Q8S2S0 THEHA	Q8S2S0 thellungiel
37	67.5	15.2	377	1	PGES2 MACFA	Q9n0a4 macaca fasc
38	67.5	15.2	413	2	Q8Y3J5 LISMO	Q8Y3J5 listeria mo
39	67.5	15.2	566	2	Q7IVS1 LISMF	Q7IVS1 listeria mo
40	67.5	15.2	616	2	Q5B1F2 EMENI	Q5B1F2 aspergillus
41	67	15.1	105	2	Q5E184 9VIRU	Q5E184 potato mop-
42	67	15.1	106	2	Q5E186 9VIRU	Q5E186 potato mop-
43	67	15.1	312	2	Q5LEH7 BACFN	Q5leH7 bacteroides
44	67	15.1	440	2	Q81UF5 BACAN	Q81uf5 bacillus an
45	67	15.1	1243	2	Q53MF0 ORYSA	Q53mf0 oryza sativ

RESULT 1

ID	MSAP HUMAN	STANDARD;	PRT;	182 AA.
AC	O9Y2B0; O9UHE9;			
DT	25-OCT-2004 (Rel. 45, Created)			
DT	25-OCT-2004 (Rel. 45, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	MIR-interacting saposin-like protein precursor (Transmembrane protein 4) (Putative secreted protein ZSIGN9)			
GN	Name=TWEM4; Synonym=MSAP, ZSIGN9; ORFNames=UNQ1943/PRO4426;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo			
OX	NCBI_TaxID=9606;			
UN	[1]			
RP	NUCLEOTIDE SEQUENCE (ISOFORM 1).			
RC	TISSUE=Gastric adenocarcinoma;			
RX	MEDLINE=99173880; PubMed=10072769; DOI=10.1016/S0378-1119(99)00004-9;			
RA	Yokoyama-Kobayashi M., Yamaguchi T., Sekine S., Kato S.;			
RT	"Selection of cDNAs encoding putative type II membrane proteins on the cell surface from a human full-length cDNA bank.";			
RL	Gene 228:161-167(1999).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE (ISOFORM 1), INTERACTION WITH MYLIP, AND TISSUE SPECIFICITY.			
RX	PubMed=12826659; DOI=10.1074/jbc.M306271200;			
RA	Bornhauser B.C., Olsson P.-A., Lindholm D.;			
RT	"MSAP is a novel MIR-interacting protein that enhances neurite outgrowth and increases myosin regulatory light chain.";			
RL	J. Biol. Chem. 278:35412-35420(2003).			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE (ISOFORM 2).			
RA	Sheppard P., Jelinek L., Whitmore T., Blumberg H., Lehner J.,			
RA	O'Hara P.;			
RT	"Homo sapiens putative secreted protein.";			
RL	Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).			
RX	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;			
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,			
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,			
RA	Eaton D., Foster J.S., Grimaldi C., Gu Q., Hase P.E., Heidens S.,			
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,			
RA	Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,			
RA	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,			
RA	Vandlen R.L., Watanabe C., Wicand D., Woods K., Xie M.-H.,			
RA	Yanura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,			
RA	Wood W.I., Godowski P.J., Gray A.M.;			
RT	"The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment.";			
RL	Genome Res. 13:2265-2270(2003).			
RN	[5]			

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -1- FUNCTION: Positive regulator of neurite outgrowth (By similarity).
CC -1- SUBUNIT: Interacts with MLLP/MIR (By similarity).
CC -1- SIMILARITY: Contains 1 saposin B-type domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC -----
DR EMBL; AF186115; AAF01433.1; -; mRNA.
DR EMBL; AK007914; BAB25346.1; -; mRNA.
DR EMBL; AK013014; BAB28597.1; -; mRNA.
DR EMBL; AK013568; BAB28909.1; -; mRNA.
DR EMBL; AK019927; BAB31921.1; -; mRNA.
DR EMBL; BC008261; AAH08261.1; -; mRNA.
DR Ensembl; ENSMUSG0000025381; Mus musculus.
DR MGI; MGI-1928477; Tmem4.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR000886; ER_target_S.
DR InterPro; IPR008139; SaposinB.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS50015; SAP_B; 1.
KW Signal.
FT CHAIN 1 20 Potential.
FT SIGNAL 21 182 MIR-interacting saposin-like protein.
FT DOMAIN 24 175 Saposin B-type.
FT MOTIF 179 182 Prevents secretion from ER (Potential).
SQ SEQUENCE 182 AA; 20767 MW; 83E54E7F01EB9B87 CRC64;
Query Match 81.3%; Score 361; DB 1; Length 182;
Best Local Similarity 97.1%; Pred. No. 2.9e-31;
Matches 67; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MKGNGWLLALLGLGTAWARRSODLHCGACRALVDELEWEIAQVDPKKTQMGSPFRNP 60
Db 1 MKGNGWLLALLGLVLTAWARRSODLHCGACRALVDELEWEIAQVDPKKTQMGSPFRNP 60
Qy 61 DGSQSVVEV 69
Db 61 DGSQSVVEV 69
RESULT 3
Q6GPD6_XENLA
ID Q6GPD6_XENLA PRELIMINARY; PRT; 184 AA.
AC Q6GPD6_XENLA
DT 03-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MGC80474 protein.
GN Name=MGC80474;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22380257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.,
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
Dev. Dyn. 225:384-391 (2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RA Klein S., Gerhard D.S.,
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073204; AAH73204.1; -; mRNA.
DR InterPro; IPR000886; ER_target_S.
DR InterPro; IPR008139; SaposinB.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN 1.
SQ SEQUENCE 184 AA; 21039 MW; 1BDED5D398918E3E CRC64;
Query Match 57.0%; Score 253; DB 2; Length 184;
Best Local Similarity 74.6%; Pred. No. 2e-19;
Matches 47; Conservative 9; Mismatches 7; Indels 0; Gaps 0;
Qy 6 WLALLGALGTAWARRSODLHCGACRALVDELEWEIAQVDPKKTQMGSPFRNP 65
Db 10 FLPIVLVSLVGYVCARRGQDVHCGACRALVDELEWEISQVDPKKTQMGSPFRNP 69
Qy 66 VVE 68
Db 70 VIE 72
RESULT 4
Q4KLC8_XENLA
ID Q4KLC8_XENLA PRELIMINARY; PRT; 184 AA.
AC Q4KLC8_XENLA
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]

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RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek G.J., Gunaratne P.H.,
Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallus D.E.,
Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole;
RX Klein S., Gerhard D.S.;
Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC099289; AA099289.1; -; mRNA.
KW Hypothetical protein.
SQ SEQUENCE 184 AA; 21007 MW; CCB7184926917596 CRC64;
Query Match 57.0%; Score 253; DB 2; Length 184;
Best Local Similarity 73.4%; Pred. No. 2e-19;
Matches 47; Conservative 9; Mismatches 8; Indels 0; Gaps 0;
Qy 6 WLALLGALGTAWARRSQDLHCACRALVDELEWEIAQVDPKKTQMGSFRINPDGQS 65
Db 10 FLPIVLVSLGCVCCARRGQDVHCACRALVDELEWEISQVDPKKTQKGSFRINPDGQS 69
Qy 66 VVEV 69
Db 70 VIEV 73
RESULT 5
Q4SS46.TETNG PRELIMINARY; PRT; 184 AA.
AC Q4SS46;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 11 SCFA14479, whole genome shotgun sequence.
GN ORNames=GSTNG0001361400;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Jailon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dosat C., Segurens B.,
Pasiva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
Anthonard V., Jubin C., Castell V., Katinka M., Vacherie B.,
Blemond C., Skall J., Cattolico L., Poulain J., De Berardinis V.,
Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
Parra G., Lardier G., Chappie C., McKernan K.J., McEwan P., Bosak S.,
Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
Wincker P., Lander E.S., Weissbach J., Roest Crollius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RL the early vertebrate proto-karyotype.";
RN Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CA001014479; CAF96536.1; -; Genomic DNA.
SQ SEQUENCE 184 AA; 20614 MW; 89CE0010ED99D9B9 CRC64;
Query Match 48.5%; Score 215.5; DB 2; Length 184;
Best Local Similarity 71.9%; Pred. No. 2.5e-15;
Matches 46; Conservative 6; Mismatches 9; Indels 3; Gaps 2;
Qy 8 ALLLGLALL--GTAWARRSQDLHCACRALVDELEWEIAQVDPKKTQMGSFRINPDGQS 65
Db 11 SLILLFLLFGQA-ARQGQDMKGCACRALVDELEWEIAISQVDPKKTQKGSFRINPDGQS 69
Qy 66 VVEV 69
Db 70 IREV 73
RESULT 6
Q5M7D4.XENLA PRELIMINARY; PRT; 181 AA.
AC Q5M7D4;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE LOC496234 protein.
GN Name=LOC496234;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek G.J., Gunaratne P.H.,
Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RA Klein S., Gerhard D.S.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC088697; AAH8697.1; -; mRNA.
DR InterPro; IPR000886; ER target S.
DR PROSITE; PS00014; ER TARGET; UNKNOWN 1.
SQ SEQUENCE 181 AA; 20706 MW; B2B8641C5413F924 CRC64;

Query Match 36.4%; Score 161.5; DB 2; Length 181;
Best Local Similarity 54.5%; Pred. No. 2e-09;
Matches 36; Conservative 12; Mismatches 9; Indels 9; Gaps 3;

QY 7 LALLL--GALLGTAW-----ARRSDLHCGACALVDELEWETAQVDPKKTQMGSFRI 58
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
1 MAILLHFGVLI-TAFLSHVGEGRDPILYCGACALVDELLYEIRKNPKKTVDVGSFRI 59

QY 59 NPDGSQ 64
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
60 SPDGKQ 65

RESULT 7
Q61L56 CAEBR PRELIMINARY; PRT; 192 AA.
AC Q61L56;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein CBG09065.
GN Names=CBG09065;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RG The C.briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAC0100041; CAE64378.1; -; Genomic DNA.
KW Hypothetical protein.
SQ SEQUENCE 192 AA; 21152 MW; 619ADEC09CB411D5 CRC64;

Query Match 28.3%; Score 125.5; DB 2; Length 192;
Best Local Similarity 50.0%; Pred. No. 1.9e-05;
Matches 28; Conservative 8; Mismatches 19; Indels 1; Gaps 1;

QY 9 LLLGALLGTAWARRSDPLHCGACALVDELEWETAQVDPKKTQMGSFRI 64
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
9 ILLSSIGFNSASVS-SLECCAGSLLVTHPELKIAGVDPKPKKIEVGSFRVPTGEQ 63

RESULT 8
Q95QNI CAEEL PRELIMINARY; PRT; 193 AA.
AC Q95QNI;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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DE Hypothetical protein F01F1.15.
GN ORFNames=F01F1.15;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology."
RL Science 282:2012-2018 (1998).
DR EMBL; U13070; AK67223.1; -; Genomic DNA.
DR Ensembl; F01F1.15; Caenorhabditis elegans.
DR WormBase; WBGene00017169; F01F1.15.
DR WormPep; F01F1.15; CE26884.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 193 AA; 21112 MW; 072306588AF3C067 CRC64;

Query Match 27.7%; Score 123; DB 2; Length 193;
Best Local Similarity 59.0%; Pred. No. 3.5e-05;
Matches 23; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 26 LHCGACALVDELEWETAQVDPKKTQMGSFRI 64
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
24 LECCAGSLLVTHPELKIAVDPKPKKIEVGSFRVPTGDQ 62

RESULT 9
Q9V5F4 DROME PRELIMINARY; PRT; 189 AA.
AC Q9V5F4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE CG12918-PA (GH10427p).
GN ORFNames=CG12918;
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananthanades P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt J., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler K., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Neison D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M.,
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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandier M., Choise N., Claudel-Renard C., Cunac S., Damange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Siguer P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL: AL646071; CAD16417.1; -; Genomic_DNA.
KW Complete proteome; Lipoprotein.
SQ SEQUENCE 146 AA; 15350 MW; 784620C8F060D589 CRC64;

Query Match 17.0%; Score 75.5; DB 2; Length 146;
Best Local Similarity 28.6%; Pred. No. 4.2;
Matches 22; Conservative 14; Mismatches 28; Indels 13; Gaps 3;

Oy 6 WLALLGALLGTAWARRSQDLHCACRALVDELEWEIAQVDPKKTQMGSPRINPDGSGS 65
Db 8 WTAALMG-LGVCAIAAQDIPVGTCPRMVQG-----AEIDGVMOQVSGTACLOPDGTWQ 60

Oy 66 VVEVTVTVPKNAHSG 82
Db 61 MADGTT-----VAYAG 71

RESULT 12
O67K51_SYNTH
ID Q67K51_SYNTH PRELIMINARY; PRT; 327 AA.
AC Q67K51;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Cation efflux system protein.
GN OrderedLocustNames=STH2964;
OS Symbiobacterium thermophilum.
OC Bacteria; Actinobacteria; Symbiobacterium.
OX NCBI_TaxID=2734;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=IAM14863;
RX PubMed=15383646; DOI=10.1093/nar/gkh830;
RA Ueda K., Yamashita A., Ishikawa J., Shimada M., Watsuji T.,
RA Morimura K., Ikeda H., Hattori M., Beppu T.;
RT "Genome sequence of Symbiobacterium thermophilum, an uncultivable bacterium that depends on microbial commensalism.";
RL Nucleic Acids Res. 32:4937-4944(2004).
DR EMBL: AP006840; BAD41947.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008324; P:cation transporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR002524; C:cation efflux.
DR Pfam; PF01545; C:cation efflux; 1.
DR TIGRFAMs; TIGR01297; CDF; 1.
KW Complete proteome.
SQ SEQUENCE 327 AA; 34193 MW; 3E1CD40918B6097B CRC64;

Query Match 17.0%; Score 75.5; DB 2; Length 327;
Best Local Similarity 35.8%; Pred. No. 9.7;
Matches 29; Conservative 9; Mismatches 32; Indels 11; Gaps 4;

Oy 3 GWG-----LALLGALLG-TAWARRSQDLHC-----GACRALVDELEWEIAQVDPKKTQ 53
Db 208 GWRWADPLAGLTVAAALARTAWSTGSEAAHMLMDGFPADRARAALAEVVLGVQGTGTVQ 266

Oy 54 GSFRINPDGSGSVVEVTVP 74
Db 267 -SLRRLMGSRVHDVTVLVP 286

RESULT 13
O94RE3_LITFO
ID Q94RE3_LITFO PRELIMINARY; PRT; 299 AA.
AC Q94RE3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE NADH dehydrogenase subunit 1.
GN Name=ND1;
OS Lithobius forficatus.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Myriapoda; Chilopoda;
OC Pleurostigmophora; Lithobiomorpha; Lithobiidae; Lithobius.
OX NCBI_TaxID=7552;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21441907; PubMed=11557978; DOI=10.1038/35093090;
RA Hwang U., Friedrich M., Choe C., Kim W.;
RT "Mitochondrial protein phylogeny joins myriapods with chelicerates.";
RL Nature 413:154-157(2001).
DR EMBL: AJ270997; CAC69948.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR001694; P:electron transport; IEA.
DR Pfam; PF00146; NADHdh; 1.
DR PROSITE; PS00667; COMPLEX1_ND1_1; 1.
KW Mitochondrion.
SQ SEQUENCE 299 AA; 33719 MW; 0927CDD757ED7878 CRC64;

Query Match 16.7%; Score 74; DB 2; Length 299;
Best Local Similarity 28.6%; Pred. No. 13;
Matches 18; Conservative 15; Mismatches 24; Indels 6; Gaps 2;

Oy 3 GW-----GWLALLGALLGTAWARRSQDLHCACRALVDELEWEI--AQVDPKKTQMGSP 56
Db 98 GWLYFLSFIAVSVYAIIGSGWFSKVALGALRAVAQTISYEVCALMWIIMLVSVGSF 157

Oy 57 RIN 59
Db 158 NLN 160

RESULT 14
PGES2_HUMAN
ID PGES2_HUMAN STANDARD; PRT; 377 AA.
AC Q9H7Z7; Q53EW9; Q5SYV6; Q96G10; Q96GL2;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Prostaglandin E synthase-2 (EC 5.3.99.3) (Microsomal prostaglandin E synthase-2) (mPGES-2) [Contains: Prostaglandin E synthase-2, truncated form].
GN Name=PTGES2; Synonyms=PGES2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Embryo;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Oobayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
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RA Yamazaki M., Ninomiya K., Ishibaishi T., Yamaehita H., Murakawa K.,
RA Fujimori K., Tanai H., Kinata M., Watanabe M., Hiraoka S., Chiba Y.,
RA Hishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hota T.,
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Inoue N., Mueahino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara T., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Koniya M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki H., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Komatsu T.,
RA Togaishi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamaehita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.";
RL Nat. Genet. 36:40-45(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed:15164053; DOI=10.1038/nature02465;
RA Humphray S.J., Oliver K., Hunt A.R., Plumb R.W., Loveland J.E.,
RA Howe K.L., Andrews T.D., Searle S., Hunt S.E., Scott C.E., Jones M.C.,
RA Ainscough R., Almeida J.P., Ambrose K.D., Ashwell R.I.S.,
RA Babbage A.K., Babbage S., Baguley C.L., Bailey J., Banerjee R.,
RA Barker D.J., Barlow K.P., Bates K., Beasley H., Beasley O., Bird C.P.,
RA Bray-Allen S., Brown A.J., Brown J.Y., Burford D., Burrill W.,
RA Burton J., Carder C., Carter N.P., Chapman J.C., Chen Y., Clarke G.,
RA Clark S.Y., Clee C.M., Clegg S., Collier R.E., Corby N., Crosier M.,
RA Cummings A.T., Davies J., Dhani P., Dunn M., Dutta I., Dyer L.W.,
RA Earthwail M.E., Faulkner L., Fleming C.J., Frankish A.,
RA Frankland J.A., French L., Fricker D.G., Garner P., Garnett J.,
RA Ghori J., Gilbert J.G.R., Gilson C., Grafham D.V., Gribble S.,
RA Griffiths C., Griffiths-Jones S., Grocock R., Guy J., Hall R.E.,
RA Hammond S., Harley J.L., Harrison E.S.I., Hart E.A., Heath P.D.,
RA Henderson C.D., Hopkins B.L., Howard P.J., Howden P.J., Huckle E.,
RA Johnson C., Johnson D., Joy A.A., Kay M., Keenan S., Kershaw J.K.,
RA Kimberley A.M., King A., Knights A., Laird G.K., Langford C.,
RA Lawlor S., Leongamornlert D.A., Leversha M., Lloyd C., Lloyd D.M.,
RA Lovell J., Martin S., Mashreghi-Mohammadi M., Matthews L., McLaren S.,
RA McLay K.E., McMurray A., Milne S., Nickerson T., Nisbett J.,
RA Nordsiek G., Pearce A.V., Peck A.I., Porter K.M., Pandian R.,
RA Pelan S., Phillimore B., Povey S., Ramsey Y., Rand V., Scharfe M.,
RA Seward H.K., Showkneen R., Sims S.K., Skuce C.D., Smith M.,
RA Steward C.A., Swarbreck D., Symamore N., Tester J., Thorpe A.,
RA Tracey A., Tromans A., Thomas D.W., Wall M., Wallis J.M., West A.P.,
RA Whitehead S.L., Willey D.L., Williams S.A., Wilming L., Wray P.W.,
RA Young L., Ashurst J.L., Coulson A., Blocker H., Durbin R.,
RA Sulston J.E., Hubbard T., Jackson M.J., Bentley D.R., Beck S.,
RA Rogers J., Dunham I.;
RT "DNA sequence and analysis of human chromosome 9";
RL Nature 429:369-374(2004).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Brain and Lung;
RX PubMed:22388257; PubMed:12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Colling P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Saplaton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Munzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahay J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP TISSUE SPECIFICITY.
RX PubMed:11866447; DOI=10.1006/bbr.2002.6531;
RA Tanikawa N., Ohmiya Y., Ohkubo H., Hashimoto K., Kangawa K.,
RA Kojima M., Ito S., Watanabe K.;
RT "Identification and characterization of a novel type of membrane-
RT associated prostaglandin E synthase.";
RL Biochem. Biophys. Res. Commun. 291:884-889(2002).
RN [6]
RP COFACTOR, AND MUTAGENESIS OF CYS-110 AND CYS-113.
RX PubMed:12804604;
RA Watanabe K., Ohkubo H., Niwa H., Tanikawa N., Koda N., Ito S.,
RA Ohmiya Y.;
RT "Essential 110Cys in active site of membrane-associated prostaglandin
RT E synthase-2.";
RL Biochem. Biophys. Res. Commun. 306:577-581(2003).
RN [7]
RP CLEAVAGE, AND SUBCELLULAR LOCATION.
RX PubMed:12835322; DOI=10.1074/jbc.M305108200;
RA Murakami M., Nakaehima K., Kamei D., Masuda S., Ishikawa Y., Ishii T.,
RA Ohmiya Y., Watanabe K., Kudo I.;
RT "Cellular prostaglandin E2 production by membrane-bound prostaglandin
RT E synthase-2 via both cyclooxygenases-1 and -2.";
RL J. Biol. Chem. 278:37937-37947(2003).
RN [8]
RP INTERACTION WITH EXOSC10.
RX PubMed:15231747; DOI=10.1101/gr.2122004;
RA Lehner B., Sanderon C.M.;
RT "A protein interaction framework for human mRNA degradation.";
RL Genome Res. 14:1315-1323(2004).
CC -1- FUNCTION: Isomerase that catalyzes the conversion of unstable
CC intermediate of prostaglandin E2 H2 (PGH2) into the more stable
CC prostaglandin E2 (PGE2) form. May also have transactivation
CC activity toward IFN-gamma (IFNG), possibly via an interaction with
CC CEBPB; however, the relevance of transcription activation activity
CC remains unclear.
CC -1- CATALYTIC ACTIVITY: (5Z,13E)-(15S)-9-alpha,11-alpha-epidioxo-15-
CC dihydroxyprosta-5,13-dienoate = (5Z,13E)-(15S)-11-alpha,15-
CC dihydroxy-9-oxoprost-5,13-dienoate.
CC -1- COFACTOR: Dihydrolipoic acid.
CC -1- PATHWAY: Prostaglandin biosynthesis.
CC -1- SUBUNIT: Homodimer. May interact with CEBPB (By similarity).
CC -1- SUBCELLULAR LOCATION: Membrane-bound and soluble. Synthesized as a
CC Golgi membrane-bound protein, which is further cleaved into the
CC predominant soluble truncated form. The truncated form is
CC cytoplasmic and is enriched in the perinuclear region.
CC -1- TISSUE SPECIFICITY: Widely expressed. Expressed in the heart,
CC including apex, inter-ventricular septum, both atria and
CC ventricles, but not in the aorta. Also expressed in fetal heart.
CC Detected in various regions of the brain: cerebellum; occipital,
CC frontal and parietal lobes. Also expressed in the lymph nodes,
CC skeletal muscle, kidney and trachea, but not in the thymus or
CC lung. Overexpressed in colorectal cancer.
CC -1- SIMILARITY: Belongs to the GST superfamily.
CC -1- CAUTION: Ref.3 (CA113822) sequence differs from that shown due to
CC erroneous gene model prediction.
CC -----
CC This Swiss-Brot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	123	27.7	580	2	T15949	hypothetical prote
2	70.5	15.9	375	2	F70691	hypothetical prote
3	69.5	15.7	566	2	AF1803	Sucrose phosphoryl
4	69	15.5	181	2	E83342	hypothetical prote
5	68	15.3	162	2	F82493	hypothetical prote
6	67.5	15.2	377	2	JC7977	membrane-associate
7	67.5	15.2	413	2	AG1429	Sucrose phosphoryl
8	65.5	14.8	233	2	A96495	unknown protein [i
9	65.5	14.8	1040	1	A83306	alpha-mannosidase
10	64.5	14.5	185	2	G84341	hypothetical prote
11	64.5	14.5	325	2	T11116	NADH2 dehydrogenas
12	63.5	14.3	322	2	S01499	NADH2 dehydrogenas
13	63.5	14.3	323	2	T11793	NADH2 dehydrogenas
14	63.5	14.3	323	2	A32484	NADH2 dehydrogenas
15	63.5	14.3	335	2	G96607	probable galactinol
16	63.5	14.3	428	2	F83990	lactose transport
17	63.5	14.3	528	2	T10622	hypothetical prote
18	63	14.2	293	2	G85794	heat shock protein
19	63	14.2	293	2	C90946	heat shock protein
20	63	14.2	754	2	S75113	catalase [EC 1.1.1.
21	63	14.2	3175	1	RRWVEV	genome polyprotein
22	62.5	14.1	151	2	T34640	probable integral
23	62.5	14.1	308	2	AE2359	hypothetical prote
24	62	14.0	98	2	S03386	antigen (clone 22)
25	62	14.0	281	2	G87451	hypothetical prote
26	62	14.0	293	2	AD0728	heat shock protein
27	62	14.0	440	2	T15352	hypothetical prote
28	62	14.0	877	2	I48967	brain-specific kin
29	62	14.0	893	2	S51603	receptor-like tyro

Y, GENE: KAZOTSC

Db 120 LDFHALPYQVVENPVLRAEIKFSSYRKVPILVAQEGSSQQLNDSSVII 169

RESULT 7

AG1429

Sucrose phosphorylase homolog lmo2840 [imported] - Listeria monocytogenes (strain EGD-e)

C;Species: Listeria monocytogenes

C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 05-Oct-2004

C;Accession: AG1429

R;Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A;Authors: Krefft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mak, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AG1429

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-413 <GLA>

A;Cross-references: UNIPROT:Q8Y3J5; UNIPARC:UPI000000CF250; GB:NC_003210; PIDN:CAD01053.1

A;Experimental source: strain EGD-e

C;Genetics:

A;Gene: lmo2840

C;Superfamily: sucrose phosphorylase

Query Match 15.2%; Score 67.5; DB 2; Length 413;

Best Local Similarity 45.0%; Pred. No. 9.8;

Matches 18; Conservative 6; Mismatches 7; Indels 9; Gaps 1;

Qy 33 ALVDELEWEIAQVDPKKTQMGSPRINPDGSQSVVEVTVT 72

Db 201 ALVNDLEEGALV-----SYKQNPDGSKSPYEINVT 231

RESULT 8

A96495

unknown protein [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: A96495

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federapfel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizart, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: A96495

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-233 <STO>

A;Cross-references: UNIPROT:Q9C8E9; UNIPARC:UPI000000A96F7; GB:AE005173; NID:g11141996; H

C;Genetics:

A;Gene: T8D8.4

A;Map position: 1

Query Match 14.8%; Score 65.5; DB 2; Length 233;

Best Local Similarity 33.3%; Pred. No. 8.9;

Matches 14; Conservative 10; Mismatches 17; Indels 1; Gaps 1;

Qy 23 SQDLHCGACRALVDELEWEIAQVDPKKTQMGSPRINPDGSQ 64

Db 20 SVDDKCAACNAVABELEQLLKEKPRNHLDMRN-RLMSKGQR 60

RESULT 9

A38306

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - Florometra serratissima mitochond

C;Species: mitochondrion Flormetra serratissima

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C;Accession: T11116

R;Scouras, A.; Smith, M.J.

Submitted to the EMBL Data Library, February 1998

A;Description: The complete mitochondrial genome of the crinoid Flormetra serratissima.

alpha-mannosidase (EC 3.2.1.24) - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004

C;Accession: A38306

R;Bischoff, J.; Moremen, K.; Lodish, H.F.

J. Biol. Chem. 265, 17110-17117, 1990

A;Title: Isolation, characterization, and expression of cDNA encoding a rat liver endoplasmic reticulum alpha-mannosidase.

A;Reference number: A38306; MUID:91009139; PMID:2211613

A;Accession: A38306

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1040 <BIS>

A;Cross-references: UNIPROT:P11139; UNIPARC:UPI000012EAC9; GB:M57547; GB:J05632; NID:920

C;Superfamily: Saccharomyces alpha-mannosidase

C;Keywords: glycosidase; hydrolase

Query Match 14.8%; Score 65.5; DB 1; Length 1040;

Best Local Similarity 32.0%; Pred. No. 44;

Matches 24; Conservative 3; Mismatches 25; Indels 23; Gaps 3;

Qy 28 CGACRALVDELEWEIAQVDPKKTQMGSPRINPDGSQ-----SVVEVTVT 72

Db 386 CGIKRFLTKLSMNLVNSPPHHTF----FWEGLDGSQVLVHFPFGDSYGMQGSVEEVLT 441

Qy 73 VPPN-----KVAHSGF 83

Db 442 VTNRDKGRTNHSGF 456

RESULT 10

G84341

hypothetical protein Vng1906h [imported] - Halobacterium sp. NRC-1

C;Species: Halobacterium sp. NRC-1

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C;Accession: G84341

R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithausen, B.; Keller, K.; Cruz, R.; Danison, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon, Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li, A.; Title: Genome sequence of Halobacterium species NRC-1.

A;Reference number: A84160; MUID:20504483; PMID:11016950

A;Accession: G84341

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-185 <STO>

A;Cross-references: UNIPROT:Q9HNK1; UNIPARC:UPI00000639D1; GB:AE004437; NID:g10581348; P

C;Genetics:

A;Gene: VNG1906H

C;Superfamily: Escherichia coli hypothetical protein b4140

Query Match 14.5%; Score 64.5; DB 2; Length 185;

Best Local Similarity 25.3%; Pred. No. 9;

Matches 22; Conservative 13; Mismatches 33; Indels 19; Gaps 3;

Qy 5 GW-----LALLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKT-----IQ 52

Db 30 GWOLTVALVLTALLGLTFVRAEG-----RATLSRLQASVARGDPPTNELVDGGLLIA 82

Qy 53 MGSFRINPDGSQSVVEVTVPENKVA 79

Db 83 AGAFLTPGLVTDALGLFIVIPTRVA 109

RESULT 11

T11116

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - Flormetra serratissima mitochond

C;Species: mitochondrion Flormetra serratissima

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C;Accession: T11116

R;Scouras, A.; Smith, M.J.

Submitted to the EMBL Data Library, February 1998

A;Description: The complete mitochondrial genome of the crinoid Flormetra serratissima.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: G96607
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-335 <STO>
A;Cross-references: UNIPROT:Q9FXB2; UNIPARC:UPI00000A96EC; GB:AE005173; NID:g9954752; PI:
C;Genetics:
A;Gene: F25p12.95
A;Map position: 1

Query Match 14.3%; Score 63.5; DB 2; Length 335;
Best Local Similarity 27.5%; Pred. No. 22;
Matches 19; Conservative 11; Mismatches 34; Indels 5; Gaps 3;
QY 19 WARESQDLHCGACRALVDELEWEIAQVDPKXTI--QMGSPRINPDGS--QSVVEVTVTVP 74
Db 151 WS-HSPQYKIGYCQCPDKVTWPEAKLGPKPPLYFNAGMFVYEPNLSTYHNLLETVKIVP 209
QY 75 PNKVAHSGF 83
Db 210 PTLFAEQDF 218

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GenCore version 5.1.8
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OM protein - protein search, using sw model

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(without alignments)
149.176 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/iaa/H-COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/pCTUS-COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE-COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	444	100.0	84	2	US-09-663-600A-204
2	444	100.0	85	2	US-09-716-129-63
3	410.5	92.5	97	2	US-09-663-600A-110
4	369	83.1	182	2	US-09-663-600A-205
5	369	83.1	208	2	US-09-949-016-8023
6	209.5	47.2	86	2	US-09-663-600A-111
7	109.5	24.7	419	2	US-09-893-737-106
8	96	21.6	197	2	US-09-270-767-44025
9	73	16.4	173	2	US-09-902-540-14840
10	69	15.5	803	2	US-09-252-991A-23614
11	66.5	15.0	260	2	US-09-070-526-2
12	66.5	15.0	260	2	US-09-008-271A-7
13	66.5	15.0	260	2	US-09-618-259-7
14	66.5	15.0	260	2	US-09-968-415-7
15	66.5	15.0	260	2	US-09-999-833A-395
16	66.5	15.0	260	2	US-10-020-445A-395
17	65.5	14.8	337	2	US-09-540-236-3792
18	65	14.6	4019	2	US-09-854-133-425
19	64	14.4	792	2	US-09-543-681A-6617
20	63.5	14.3	291	2	US-09-902-540-12562
21	63.5	14.3	335	2	US-09-810-506-2
22	63	14.2	149	2	US-09-270-767-47049
23	62	14.0	877	1	US-08-673-789-2
24	62	14.0	928	1	US-08-442-248-2
25	62	14.0	928	1	US-08-440-815-2
26	62	14.0	928	1	US-08-486-449-2
27	62	14.0	928	2	US-08-578-684-2

28	62	14.0	1005	1	US-08-469-537A-103	Sequence 103, App
29	61.5	13.9	123	2	US-09-252-991A-25180	Sequence 25180, A
30	61.5	13.9	305	2	US-09-248-796A-20913	Sequence 20913, A
31	61.5	13.9	354	2	US-09-270-767-44204	Sequence 44204, A
32	61	13.7	106	2	US-09-107-532A-6515	Sequence 6515, Ap
33	61	13.7	376	2	US-09-464-535-42	Sequence 42, Appl
34	61	13.7	1006	2	US-09-949-016-8421	Sequence 8421, Ap
35	61	13.7	1006	2	US-09-949-016-8530	Sequence 8530, Ap
36	60.5	13.6	271	1	US-08-447-554-4	Sequence 4, Appl
37	60.5	13.6	271	1	US-08-448-160-4	Sequence 4, Appl
38	60.5	13.6	1115	2	US-09-435-376-5	Sequence 5, Appl
39	60	13.5	267	1	US-08-793-490-11	Sequence 11, Appl
40	60	13.5	296	2	US-09-949-016-10758	Sequence 10758, A
41	60	13.5	308	2	US-09-976-594-909	Sequence 909, App
42	60	13.5	308	2	US-09-919-039-360	Sequence 360, App
43	60	13.5	333	2	US-09-949-016-7304	Sequence 7304, Ap
44	59.5	13.4	119	2	US-10-101-464A-832	Sequence 832, App
45	59.5	13.4	120	2	US-09-228-986-128	Sequence 128, App

ALIGNMENTS

RESULT 1
US-09-663-600A-204
; Sequence 204, Application US/09663600A
; Patent No. 6573068
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
; FILE REFERENCE: 31.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/663,600A
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/099,273
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent.pm
; SEQ ID NO 204
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -20...-1
US-09-663-600A-204

Query Match 100.0%; Score 444; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 2e-49;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MKGHWLALLGALLGTAWARRSODLHCGACRALVDELEWIAQVDPKTTQMGSRINP	60
Db	1	MKGHWLALLGALLGTAWARRSODLHCGACRALVDELEWIAQVDPKTTQMGSRINP	60
Qy	61	DGSQSVVEVTVPNKAHSGF	83
Db	61	DGSQSVVEVTVPNKAHSGF	83

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RESULT 2
US-09-716-129-63
; Sequence 63, Application US/09716129
; Patent No. 6632920
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 36 Human Secreted Proteins
; FILE REFERENCE: P2025P1
; CURRENT APPLICATION NUMBER: US/09/716,129
; CURRENT FILING DATE: 2000-11-17
; PRIOR FILING DATE: 2000-11-17
; PRIOR FILING DATE: 60/076,053
; PRIOR FILING DATE: 1998-02-26
; PRIOR FILING DATE: 60/076,057
; PRIOR FILING DATE: 1998-02-26
; PRIOR FILING DATE: 60/076,052
; PRIOR FILING DATE: 1998-02-26
; PRIOR FILING DATE: 60/076,054
; PRIOR FILING DATE: 1998-02-26
; PRIOR FILING DATE: 60/076,051
; PRIOR FILING DATE: 1998-02-26
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (85)
; OTHER INFORMATION: Xaa equals stop translation
US-09-716-129-63

Query Match      100.0%; Score 444; DB 2; Length 85;
Best Local Similarity 100.0%; Pred. No. 2e-49;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MKGHWLALLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTIQMGSFRINP 60
Db      1 MKGHWLALLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTIQMGSFRINP 60

Qy      61 DGSQSVVEVTVPNNKVAHSGF 83
Db      61 DGSQSVVEVTVPNNKVAHSGF 83

RESULT 3
US-09-663-600A-110
; Sequence 110, Application US/09663600A
; Patent No. 6573068
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
; FILE REFERENCE: 31.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/663,600A
; CURRENT FILING DATE: 2000-09-15
; PRIOR FILING DATE: 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR FILING DATE: 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR FILING DATE: 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR FILING DATE: 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR FILING DATE: 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR FILING DATE: 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR FILING DATE: 60/099,273
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent.pm
; SEQ ID NO 205
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -20...-1
US-09-663-600A-205

Query Match      83.1%; Score 369; DB 2; Length 182;
Best Local Similarity 100.0%; Pred. No. 2.4e-39;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MKGHWLALLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTIQMGSFRINP 60
Db      1 MKGHWLALLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTIQMGSFRINP 60

Qy      61 DGSQSVVEV 69
Db      61 DGSQSVVEV 69

RESULT 4
US-09-663-600A-205
; Sequence 205, Application US/09663600A
; Patent No. 6573068
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
; FILE REFERENCE: 31.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/663,600A
; CURRENT FILING DATE: 2000-09-15
; PRIOR FILING DATE: 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR FILING DATE: 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR FILING DATE: 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR FILING DATE: 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR FILING DATE: 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR FILING DATE: 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR FILING DATE: 60/099,273
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent.pm
; SEQ ID NO 205
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -20...-1
US-09-663-600A-205

Query Match      83.1%; Score 369; DB 2; Length 182;
Best Local Similarity 100.0%; Pred. No. 2.4e-39;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MKGHWLALLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTIQMGSFRINP 60
Db      1 MKGHWLALLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTIQMGSFRINP 60

Qy      61 DGSQSVVEV 69
Db      61 DGSQSVVEV 69
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RESULT 5
US-09-949-016-8023
; Sequence 8023, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8023
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8023

Query Match      83.1%; Score 369; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 2.9e-39;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKGWMGLALLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTQMGSRINP 60
DB 27 MKGWMGLALLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTQMGSRINP 86

QY 61 DGSQSVVEV 69
DB 87 DGSQSVVEV 95

RESULT 6
US-09-663-600A-111
; Sequence 111, Application US/09663600A
; Patent No. 6573068
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueret, Lydie
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
; FILE REFERENCE: 31.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/663,600A
; CURRENT FILING DATE: 2000-09-15
; PRIOR FILING DATE: 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR FILING DATE: 1997-11-13
; PRIOR FILING DATE: 1997-12-17
; PRIOR FILING DATE: 1997-12-17
; PRIOR FILING DATE: 1998-02-09
; PRIOR FILING DATE: 1998-04-13
; PRIOR FILING DATE: 1998-04-13
; PRIOR FILING DATE: 1998-08-10
; PRIOR FILING DATE: 1998-08-10
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent.pm
; SEQ ID NO 111
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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; NAME/KEY: SIGNAL
; LOCATION: -20...-1
US-09-663-600A-111

Query Match      47.2%; Score 209.5; DB 2; Length 86;
Best Local Similarity 67.2%; Pred. No. 2.8e-19;
Matches 43; Conservative 3; Mismatches 15; Indels 3; Gaps 1;

QY 1 MKGWMGLALLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTQMGSRINP 60
DB 1 MKGWMGLALLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTQMGSRINP 57

QY 61 DGSQ 64
DB 58 DQSR 61

RESULT 7
US-09-893-737-106
; Sequence 106, Application US/09893737
; Patent No. 6822082
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Presnell, Scott R.
; TITLE OF INVENTION: MAMMALIAN SECRETED PROTEINS
; FILE REFERENCE: 00-41
; CURRENT APPLICATION NUMBER: US/09/893,737
; CURRENT FILING DATE: 2001-06-28
; PRIOR FILING DATE: 2001-06-28
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 106
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-893-737-106

Query Match      24.7%; Score 109.5; DB 2; Length 419;
Best Local Similarity 62.9%; Pred. No. 1.7e-05;
Matches 22; Conservative 7; Mismatches 5; Indels 1; Gaps 1;

QY 30 ACRALVDELEWEIAQVDPKKTQMGSRINPDGSG 64
DB 216 ACRALMDEIHDITKAROKKT-KVGSFRINPDGTQ 249

RESULT 8
US-09-270-767-44025
; Sequence 44025, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44025
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-44025

Query Match      21.6%; Score 96; DB 2; Length 197;
Best Local Similarity 37.9%; Pred. No. 0.00034;
Matches 22; Conservative 13; Mismatches 21; Indels 2; Gaps 1;

QY 8 ALLGLALGTA--WARRSQDLHCGACRALVDELEWEIAQVDPKKTQMGSRINPDGS 63
DB 13 ALLFGLLALAQGYSTSRVCKVCKAVVTELEEAIAKEDPHKMDVSGFRDLDAQGN 70
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RESULT 9
; Sequence 14840, Application US/0902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldmann, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 14840
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-14840

Query Match          16.4%; Score 73; DB 2; Length 173;
Best Local Similarity 26.0%; Pred. No. 0.26;
Matches 25; Conservative 7; Mismatches 18; Indels 46; Gaps 4;

QY 2 KGWGLALLGAL-LGTAWARRSQDLHCGACRALVDELEWEIAQVDPK-----48
Db 7 RGNWAGALGTLALGTAYS-----ATEAPQVAQVDPSTGQTVTPGTAPS 52

QY 49 -----KTIQMGSRINPDGQSQSVVEVTVP 75
Db 53 NTTSGTGPPTGTSTNTNPN-----TLPP 78

RESULT 10
US-09-252-991A-23614
; Sequence 23614, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23614
; LENGTH: 803
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23614

Query Match          15.5%; Score 69; DB 2; Length 803;
Best Local Similarity 28.0%; Pred. No. 6.7;
Matches 21; Conservative 12; Mismatches 26; Indels 16; Gaps 3;

QY 3 GWWGLALLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKTIQMG-----SF 56
Db 632 GWRWLAVALGTLALSALAEASMARWPAG-----WQVSDLPAAQPGQAGAQORAV 682

QY 57 RINPDGQSQSVVEVT 70
Db 683 KLQADGSQALVMEVT 697

RESULT 11
US-09-070-526-2
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```
; Sequence 2, Application US/09070526
; Patent No. 6100059
; GENERAL INFORMATION:
; APPLICANT: SOUTHAN, CHRISTOPHER
; APPLICANT: CLINKENBEARD, HELEN
; APPLICANT: BURGESS, NICOLA
; TITLE OF INVENTION: No. 6100059el Compounds
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,526
; FILING DATE: 30-APR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9711952.3
; FILING DATE: 9-JUN-1997
; APPLICATION NUMBER: EP 97309646.4
; FILING DATE: 1-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-30353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 260 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-070-526-2

Query Match          15.0%; Score 66.5; DB 2; Length 260;
Best Local Similarity 26.0%; Pred. No. 3;
Matches 26; Conservative 10; Mismatches 27; Indels 37; Gaps 6;

QY 6 WLALLGALLGTAWARRS-----ODLHCGACRALVDEL 38
Db 12 WMFL---LLGGAWAGHSRAQEDKVLGGHETQPHSQFQWQALFQQQLLCGG---VLVGG- 65

QY 39 EWEIAQV---DPKTIQMGSRFRI-NPDGQSQSVVEVTVP 74
Db 66 NWVLTAAHCKKPKYTVRLGDHSLQNKDGPQEIPIVQSIP 105

RESULT 12
US-09-008-271A-7
; Sequence 7, Application US/09008271A
; Patent No. 6203979
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Hillman, Jennifer L.
; Yue, Henry
; Guegler, Karl J.
; Corley, Neil C.
; Tang, Tom Y.
; Shah, Purvi
; TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
; NUMBER OF SEQUENCES: 24
```

```
;
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/008,271A
; FILING DATE: 16-Jan-1998
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Mohan-Peterson, Sheila
; REGISTRATION NUMBER: 41,201
; REFERENCE/DOCKET NUMBER: PF-0458 US
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
;
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 260 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: COLNNOT27
; CLONE: 1798496
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 7 :
US-09-008-271A-7
Query Match 15.0%; Score 66.5; DB 2; Length 260;
Best Local Similarity 26.0%; Pred. No. 3;
Matches 26; Conservative 10; Mismatches 27; Indels 37; Gaps 6;

Qy 6 WLALLGALLGTAWARRS-----ODLHCCACRALYDEL 38
Db 12 WMFL-----LLGGAWAGHSRAQEDKVLGGHCQPHSQPWAALFOGQQLLCG--VLVGG- 65

Qy 39 EWEIAQV---DPKKTIONGFSRI-NPDGQSQSVVEVTVP 74
Db 66 NWLTAACHKPKYTVRLGDHSLQNKDGPQEIPVQSIP 105

RESULT 13
US-09-618-259-7
; Sequence 7, Application US/09618259
; Patent No. 6642013
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: No. 6642013el Extracellular Serine Protease
; FILE REFERENCE: D6020CIP2
; CURRENT APPLICATION NUMBER: US/09/618,259
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: US 09/127,444
; PRIOR FILING DATE: 1998-08-21
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 7
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of TADG-14 protein
US-09-618-259-7
Query Match 15.0%; Score 66.5; DB 2; Length 260;

;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/008,271A
; FILING DATE: 16-Jan-1998
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Mohan-Peterson, Sheila
; REGISTRATION NUMBER: 41,201
; REFERENCE/DOCKET NUMBER: PF-0458 US
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
;
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 260 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: COLNNOT27
; CLONE: 1798496
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 7 :
US-09-008-271A-7
Query Match 15.0%; Score 66.5; DB 2; Length 260;
Best Local Similarity 26.0%; Pred. No. 3;
Matches 26; Conservative 10; Mismatches 27; Indels 37; Gaps 6;

Qy 6 WLALLGALLGTAWARRS-----ODLHCCACRALYDEL 38
Db 12 WMFL-----LLGGAWAGHSRAQEDKVLGGHCQPHSQPWAALFOGQQLLCG--VLVGG- 65

Qy 39 EWEIAQV---DPKKTIONGFSRI-NPDGQSQSVVEVTVP 74
Db 66 NWLTAACHKPKYTVRLGDHSLQNKDGPQEIPVQSIP 105

RESULT 14
US-09-968-415-7
; Sequence 7, Application US/09968415
; Patent No. 6855811
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Hillman, Jennifer L.
; Yue, Henry
; Guegler, Karl J.
; Corley, Neil C.
; Tang, Tom Y.
; Shah, Purvi
;
; TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
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; FILING DATE: 26-Sep-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/659,151
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mohan-Peterson, Sheila
; REGISTRATION NUMBER: 41,201
; REFERENCE/DOCKET NUMBER: PF-0458 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
;
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 260 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: COLNNOT27
; CLONE: 1798496
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; SEQUENCE DESCRIPTION: SEQ ID NO: 7 :
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RESULT 15

US-09-999-833A-395
Sequence 395, Application US/09999833A

Patent No. 6916648

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan
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APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
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APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
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APPLICANT: Hillan, Kenneth J.
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APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C55
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